



Blast 2 Sequences results

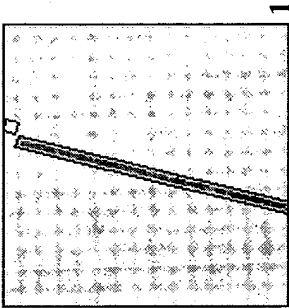
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 8509 (1 .. 8509)

Sequence 2 lc|seq_2 Length 2112 (1 .. 2112)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3857 bits (2006), Expect = 0.0
Identities = 2006/2006 (100%)
Strand = Plus / Plus



Query: 2955 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 3014

Sbjct: 1 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgtacaggggtg 60

Query: 3015 ctgcgcggagagatctctgtgtctcaggtagggcgacaatggagaggtgttagttgccccctg 3074

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|||||
Sbjct: 61 ctgcgcggagatctctggtctcaggtagggcgacaaatggagagggtgtagttgccccctg 120

Query: 3075 tatcgctctctgcgtggcgcattgggtcatcctgcccgacatatgatattccgctagag 3134
|||||
Sbjct: 121 tatcgctctctgcgtggcgcattgggtcatcctgcccgacatatgatattccgctagag 180

Query: 3135 gattactgatagtttctgcctgtcgggcttgcggccttgcgggcttgcgggcttgtc 3194
|||||
Sbjct: 181 gattactgatagtttctgcctgtcgggcttgcggccttgcgggcttgcgggcttgtc 240

Query: 3195 gggcctgtccctcttgtcccgctgtcctcactttttcacaaatcaaaaaatgggcgaagc 3254
|||||
Sbjct: 241 gggcctgtccctcttgtcccgctgtcctcactttttcacaaatcaaaaaatgggcgaagc 300

Query: 3255 ccttctgttcttatagttctttagttcatcagaaaaattacacataattatcaatagctt 3314
|||||
Sbjct: 301 ccttctgttcttatagttctttagttcatcagaaaaattacacataattatcaatagctt 360

Query: 3315 attcgcttaaaaggaggagtaattgggcgcgcaaaaggagtaattgggcgcgcaaaaggagat 3374
|||||
Sbjct: 361 attcgcttaaaaggaggagtaattgggcgcgcaaaaggagtaattgggcgcgcaaaaggagat 420

Query: 3375 aattggcgcgcaaaaggaggagtaattgggcgcgatatcgggtgtttacatggggagggaatcc 3434
|||||
Sbjct: 421 aattggcgcgcaaaaggaggagtaattgggcgcgatatcgggtgtttacatggggagggaatcc 480

Query: 3435 ccttaatcatttctcccccatgggaaagacacaacaaagtggccgcagaccgggccttcgac 3494
|||||
Sbjct: 481 ccttaatcatttctcccccatgggaaagacacaacaaagtggccgcagaccgggccttcgac 540

Query: 3495 cagacaaaaaactgtgctccctgccgaggtggcgagaggggtctatatcgcgcaatccgccc 3554
|||||
Sbjct: 541 cagacaaaaaactgtgctccctgccgaggtggcgagaggggtctatatcgcgcaatccgccc 600
```

Query: 3555 cgcctgaggcgctcaagctcatgcatttaatatagccactgcggcgccgcgatggct 3614
|||||
Sbjct: 601 cgcctgaggcgctcaagctcatgcatttaatatagccactgcggcgccgcgatggct 660

Query: 3615 gatgatgtgcgcccatgaaatcggtgctgccgacattcgcgcaatcgcgcatgaaaaac 3674
|||||
Sbjct: 661 gatgatgtgcgcccatgaaatcggtgctgccgacattcgcgcaatcgcgcatgaaaaac 720

Query: 3675 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcggtgttgacccat 3734
|||||
Sbjct: 721 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcggtgttgacccat 780

Query: 3735 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcaatagac 3794
|||||
Sbjct: 781 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcaatagac 840

Query: 3795 taccgccaggaggcaagcgcggaactcctagtacgtggacctccggaggtacattccgt 3854
|||||
Sbjct: 841 taccgccaggaggcaagcgcggaactcctagtacgtggacctccggaggtacattccgt 900

Query: 3855 cgtatggcggcgagtcgaaccactggccattctcgacctcaaacgggtattccatctc 3914
|||||
Sbjct: 901 cgtatggcggcgagtcgaaccactggccattctcgacctcaaacgggtattccatctc 960

Query: 3915 ggtagtaagtattccgtgctgctgttcacgacacgtctctagtctcgccaatcttgatcgg 3974
|||||
Sbjct: 961 ggtagtaagtattccgtgctgctgttcacgacacgtctctagtctcgccaatcttgatcgg 1020

Query: 3975 atgagcgcgaaaaacctttacggtccccgagttgcgggcgtccttgagtgccccgagggg 4034
|||||
Sbjct: 1021 atgagcgcgaaaaacctttacggtccccgagttgcgggcgtccttgagtgccccgagggg 1080

Query: 4035 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcaactggatgagatc 4094
|||||
Sbjct: 1081 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcaactggatgagatc 1140

Query: 4095 aaccatttatcgcgtctgacattgacggcaaaagccgaccaaagattggccgtagcgtggca 4154
|||||
Sbjct: 1141 aaccatttatcgcgtctgacattgacggcaaaagccgaccaaagattggccgtagcgtggca 1200

Query: 4155 agtgtgactataggctgggaagtgaagacgacccaacccgtgccaggcgcgagctggcg 4214
|||||
Sbjct: 1201 agtgtgactataggctgggaagtgaagacgacccaacccgtgccaggcgcgagctggcg 1260

Query: 4215 ggttccaaggtcggtcgagatgctcgcgagaggggcagcggaacgatagccccctcc 4274
|||||
Sbjct: 1261 ggttccaaggtcggtcgagatgctcgcgagaggggcagcggaacgatagccccctcc 1320

Query: 4275 ttcccagaagcggggcgatcacctacagtccacgttggtggagctgaaacgctctgct 4334
|||||
Sbjct: 1321 ttcccagaagcggggcgatcacctacagtccacgttggtggagctgaaacgctctgct 1380

Query: 4335 ggcagcaacaaggacaaacgatctgatgcctcagactccggcggtttctgtcgggagaga 4394
|||||
Sbjct: 1381 ggcagcaacaaggacaaacgatctgatgcctcagactccggcggtttctgtcgggagaga 1440

Query: 4395 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagattttcgcgcaaaagta 4454
|||||
Sbjct: 1441 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagattttcgcgcaaaagta 1500

Query: 4455 gggaaagtttgagttttgaggtatttcacgcgcaaatagtgtaaatactttcgtgaaaacg 4514
|||||
Sbjct: 1501 gggaaagtttgagttttgaggtatttcacgcgcaaatagtgtaaatactttcgtgaaaacg 1560

Query: 4515 atgtgcaatatagcggtaagactatgaaatacacgcgctggacaggctgcacaaagcaacgg 4574
|||||
Sbjct: 1561 atgtgcaatatagcggtaagactatgaaatacacgcgctggacaggctgcacaaagcaacgg 1620

Query: 4575 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaaatttcgggtaaaaaag 4634
|||||
Sbjct: 1621 gtgtggcgaccgcaaccatcactcggcgctaaaaaagcggtaaaaatttcgggtaaaaaag 1680

Query: 4635 atgaatctggggcattgggttatagatcctgcagaattgcacagagtgttctcctcccat 4694
|||||
Sbjct: 1681 atgaatctggggcattgggttatagatcctgcagaattgcacagagtgttctcctcccat 1740

Query: 4695 caaagaaatacacaccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacatg 4754
|||||
Sbjct: 1741 caaagaaatacacaccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacatg 1800

Query: 4755 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 4814
|||||
Sbjct: 1801 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 1860

Query: 4815 ctgatgccaggaggatcgcgacaaatggcgcgacatggccgagcgtctttcaatttcat 4874
|||||
Sbjct: 1861 ctgatgccaggaggatcgcgacaaatggcgcgacatggccgagcgtctttcaatttcat 1920

Query: 4875 caccgatgagagaggaagaccgccccctcaaaaacaaagatggtggaagatatcttgat 4934
|||||
Sbjct: 1921 caccgatgagagaggaagaccgccccctcaaaaacaaagatggtggaagatatcttgat 1980

Query: 4935 cctgggcttcaggagccttgccctta 4960
|||||
Sbjct: 1981 cctgggcttcaggagccttgccctta 2006

Score = 208 bits (108), Expect = 2e-49
Identities = 108/108 (100%)
Strand = Plus / Plus



Query: 5364 tactggcggaacacgcgatattgaggcacagggccgcacttttagagcggaagcctata 5423
|||||
Sbjct: 2005 tactggcggaacacgcgatattgaggcacagggccgcacttttagagcggaagcctata 2064

Query: 5424 acgagtaccacaaacactagaagccagattgaggaataagggaacgtg 5471

|||||
Sbjct: 2065 acgagtacacaaacactagaagccagattgaggaaaaatagggaacgtg 2112

CPU time: 0.05 user secs. 0.02 sys. secs 0.07 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 787
Number of extensions: 21
Number of successful extensions: 15
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 3
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 8509
Length of database: 12,527,565,053
Length adjustment: 28
Effective length of query: 8481
Effective length of database: 12,527,565,025
Effective search space: 106246278977025
Effective search space used: 106246278977025
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 23 (44.9 bits)